



Phylogenomics, Part II

About the workshop

Time: Week II Feb 13 – 17, 2017.

Place: The Auditorium of the Lids hus, Natural History Museum, University of Oslo

Course credits: 5 ECTS

Assessment: Written report on a provided case study within two weeks after the first week of the workshop is finished. Participation in a discussion forum with given reading assignments at the end of the second week.

Registration: Confirmation of previous registration before January 21 2017

Fee: No fee for ForBio members or associates.

Maximum number of participants: 16

Teachers: Torsten Hugo Struck (t.h.struck@nhm.uio.no), Patrick Kück (patrick_kueck@web.de)

Objectives: Advances in high-throughput sequencing and genomics have revolutionized research in evolutionary biology and systematics. The use of genomics data in phylogenetic analyses has brought new challenges in terms of data handling and analysis. This course aims to help those that have basic experience in bioinformatics and molecular phylogenetics, and have projects focused on high-throughput sequencing data and phylogenetics, to become acquainted with tools, programs and pipelines for phylogenomics and want to contact phylogenomic studies beyond the standard also addressing potentially confounding biases in their datasets.

Prerequisites: Basic knowledge of command line interaction, regular expressions, UNIX, sequence data and alignments, model-based phylogenetic analyses, model testing, Bayesian inference, is a prerequisite for participation. Pre-course exercises on command line, regex and UNIX will need to be done, submitted and passed to ensure that all participants have an equal minimum level at start of the first week. Participation of the first week to be able to participate in the second week.

Travel and accommodation: The course is arranged by the Research School in Biosystematics –

ForBio. There is no course fee for ForBio members and associates. Norwegian ForBio members will be covered for accommodation and refunded for travel expenses. ForBio will not refund travel or accommodation costs for other members and associates. See <http://www.forbio.uio.no> for more information on ForBio and membership.

Content

The workshop will consist of lectures and hands-on work aiming to provide the participants with a good working knowledge of genomic data for phylogenomics, and to become acquainted with tools, programs and pipelines for phylogenomics. To encourage discussion, participants will work in pairs most of the time. During the first week all exercises will be carried out using example data handed out by the teachers, during second week the course is more workshop-like and exercises can be done on one's own data, but if needed data will be provided by the teachers. All exercises and results can be readily transposed to individual research data.

Tentative schedule

The first week covers the basic foundation of phylogenomic studies. Lectures and labs in week II will build upon this and focus on dissecting the phylogenetic signal in the dataset. We will focus on different sources of incongruences and misleading biases. These are rogue taxa, base composition, branch length and evolutionary rate heterogeneity, saturation, paralogy, incomplete lineage sorting, horizontal gene transfer, ancestral hybridization, and contamination. Strategies for thorough sensitivity analyses in phylogenomic studies will be discussed during this week.